CLAIMS

1. A method of obtaining information about a chemically active area of a target molecule, comprising:

providing a set of substantially rigid chemical gauges;

reacting said target with a plurality of gauges of said set of gauges;

assaying a binding of said gauges with said target to obtain a plurality of assay results; and

analyzing said assay results to obtain information about said chemically active area.

2. A method according to claim 1, wherein said gauges allow rotation of moieties of said gauges.

3. A method according to claim 1, wherein said gauges are constructed using a rigid scaffold.

4. A method according to claim 1, wherein constituent atoms of said gauges do not move more than 1 Å unless at least 20Kcal/Mol are applied to the gauge.

5. A method according to claim 1, wherein analyzing comprises identifying a plurality of spatial and chemically specific bindings configurations in said target active area.

6. A method according to claim 5, wherein said configurations comprise triangular configurations.

7. A method according to claim 5, wherein identifying comprises identifying a configuration that matches a configuration of a bound gauge.

8. A method according to claim 5, wherein identifying comprises identifying a configuration that does not match a configuration of a bound gauge.

9. A method according to claim 8, wherein identifying comprises identifying by statistical analysis of said assay results.

10. A method according to claim 9, wherein identifying comprises identifying by clustering.

11. A method according to claim 5, wherein identifying comprises assuming each gauge indicates a single configuration.

12. A method according to claim 5, wherein identifying comprises assuming at least some of the gauges indicate a plurality of configurations.

13. A method according to claim 5, wherein identifying comprises classifying gauges by chemical moieties at vertexes of said configurations.

14. A method according to claim 1, comprising reconstructing a spatial map of at least part of said chemically active area, from at least two of said assay results, said part including at least four chemical binding areas.

15. A method according to claim 14, wherein said part includes at least six chemical binding areas.

16. A method according to claim 5, comprising reconstructing a spatial map of at least part of said chemically active area, from at least two of configurations, said part including at least four chemical binding points.

17. A method according to claim 16, wherein said part includes at least six chemical binding areas.

18. A method according to claim 16, wherein reconstructing comprises:
test-reconstructing a plurality of spatial maps from said configurations;
scoring said maps; and
selected a spatial map based on its score.

19. A method according to claim 16, wherein reconstructing comprises:

test-reconstructing a plurality of spatial maps from said configurations;

clustering said maps according to common substructures; and

selected a spatial map based on a relative property of a cluster it belongs to.

20. A method according to claim 19, wherein said relative property comprises size.

21. A method according to claim 16, wherein said spatial map includes enough binding points to ensure binding of a small molecule drug having a chemical profile matching the binding points.

22. A method according to claim 21, wherein said spatial map includes at least 6 binding points.

23. A method according to claim 21, wherein said spatial map includes at least 8 binding points.

24. A method according to claim 1, wherein said set of gauges comprises a set of gauges with at least 10,000 gauges.

25. A method according to claim 1, wherein said set of gauges comprises a set of gauges with at least 50,000 gauges.

26. A method according to claim 1, wherein said gauges comprise moieties arranged in spatial configurations and wherein said gauges are selected to span a virtual space of spatial chemical configurations.

27. A method according to claim 1, wherein substantially each point of virtual space that is spanned by said gauges is covered by at least two gauges.

28. A method according to claim 1, wherein substantially each point of virtual space that is spanned by said gauges is covered by at least three gauges.

29. A method according to claim 1, wherein at least 0.5% of said gauges bind with said target.

30. A method according to claim 1, wherein at least 1% of said gauges bind with said target.

31. A method according to claim 1, wherein at least 3% of said gauges bind with said target.

32. A method according to claim 1, wherein at least 50% of said gauges are defined by adding moieties to a set of fewer than 100 scaffolds.

33. A method according to claim 1, wherein at least 50% of said gauges are defined by adding moieties to a set of fewer than 50 scaffolds.

34. A method according to claim 1, wherein at least said set of gauges uses fewer than 15 different chemical moieties to define the chemical behavior of said gauges.

35. A method according to claim 1, wherein at least said set of gauges uses fewer than 10 different chemical moieties to define the chemical behavior of said gauges.

36. A method according to claim 1, wherein said assay is a functional assay.

37. A method according to claim 1, wherein said assay is a binding assay.

38. A method according to claim 1, wherein said assay is a cellular assay.

39. A method according to claim 1, wherein said assay is a flow-through assay.

40. A method according to claim 36, wherein said functional assay is performed in the presence of a natural substrate of said target.

41. A method according to claim 1, wherein said target comprises a protein including a biochemically active area adapted to engage a substrate.

42. A method according to claim 41, wherein said chemically active area comprises an area including said biochemically active area.

43. A method according to claim 41, wherein said chemically active area comprises a control area of said protein.

44. A method according to claim 1, analyzing comprises analyzing successful binding of at least 60 gauges.

45. A method according to claim 1, analyzing comprises analyzing successful binding of at least 10 gauges.

46. A method according to claim 1, analyzing comprises analyzing successful binding of at least 100 gauges.

47. A method according to claim 5, wherein identifying comprises identifying at least 40 different configurations.

48. A method according to claim 5, wherein identifying comprises identifying at least 10 different configurations.

49. A method according to claim 5, wherein identifying comprises identifying at least 100 different configurations.

50. A method according to claim 16, comprising:

comparing said map to a lead data base; and

selecting a lead from said data base for further use responsive to a semblance or lack of semblance between said lead and said map.

51. A method according to claim 16, comprising:

comparing said map to a lead data base; and

rejecting a lead from said data base for further use responsive to a semblance between said lead and said map.

52. A method according to claim 16, comprising:

constructing a lead to have a semblance to said map.

53. A method according to claim 52, wherein constructing comprises constructing using said gauges or scaffolds used to define said gauges.

54. A method according to claim 5, comprising:

comparing said configurations to a lead data base; and

selecting a lead from said data base for further use responsive to a matching of said configurations to said lead.

55. A method according to claim 5, comprising:

constructing a lead based on said configurations.

56. A method according to claim 5, comprising:

selecting at least one of said gauges as a lead for drug discovery.

57. A method according to claim 1, comprising comparing the binding of gauges with similar binding geometries to obtain steric clashing data; and

analyzing said steric clashing data to provide geometrical information about said target.

58. A method of identifying the existence of a plurality of chemical-spatial configurations in a target, comprising:

assaying the target with a plurality of gauges having know chemical-spatial configurations at vertexes thereof, to provide a plurality of assay results;

defining an array of spaces, one space for each set of chemical behaviors of the vertexes of each configuration;

indicating said results according to said spaces, to generate clusters; and

identifying the existence of a configuration in said target from said clusters.

59. A method according to claim 58, wherein indicating comprises spreading an indication responsive to a spreading function.

60. A method according to claim 59, wherein said spreading function is dependent on an estimated energy of binding of a gauge to said target.

61. A method of reconstructing a spatial shape of a chemical binding configuration of a target from a set of sub-shapes, each of which indicates a part of said binding configuration, comprising:

selecting a base from said sub-shapes;

selecting at least two sub-shapes having the property that they match each other at least along one side thereof and match said base along another side thereof;

accumulating said sub-shapes to said base; and

repeating said selecting and said accumulating until all of said sub-shapes are used or cannot be used, thereby providing a shape of a binding configuration of said target.

62. A method according to claim 61, comprising variationally repeating said selecting, accumulating and repeating using a different order of selection of sub-shapes.

63. A method according to claim 62, comprising repeating said selecting a base and said variationally repeating for a plurality of different base selections.

64. A method according to claim 63, comprising clustering a plurality of such shapes according to shared sub-component shapes.

65. A method according to claim 64, comprising selecting a sub-component shape as a resulting shape based on said clustering.

66. A method according to claim 61, wherein said sub-shapes comprise triangles.

67. A method according to claim 61, wherein said sub-shapes define chemical behavior at their vertexes and wherein two sides are said to match if the chemical behavior at their vertexes match.

68. A method according to claim 61, wherein two sides are said to match if their length is similar.

69. A method of selecting a scaffold for use in generating a part of a screening library, comprising:

providing a potential scaffold molecule including a plurality of possible attachment points for moieties;

determining a rigidity of the molecule; and

rejecting said potential scaffold molecule responsive to a lack of rigidity of said scaffold.

70. A method according to claim 69, wherein said lack of rigidity is absolute.

71. A method according to claim 69, wherein said lack of rigidity is relative to other potential scaffolds.

72. A method according to claim 69, comprising selecting a scaffold based on a number of rings thereof.

73. A method according to claim 69, comprising:

determining a plurality of gauge molecules that can be generated by adding moieties to said potential scaffold molecule;

determining for an existing library portion what spatial chemical configurations are added by said molecules; and

selecting said potential scaffold molecule if one or more significant spatial chemical configurations can be added by it to said library portion.

74. A method according to claim 73, comprising selecting a scaffold based on a number of configurations added by said scaffold.

75. A method according to claim 73, wherein said significant spatial configurations are configurations not previously provided or overlapped with,

76. A method of selecting a gauge molecule to be added to a screening library, comprising:

providing a set of chemical molecules and at least a part of a screening library;

selecting a potential gauge molecule from said set of chemical molecules;

determining a rigidity of said potential gauge molecule; and

rejecting said potential gauge molecule responsive to a lack of rigidity of said gauge molecule.

77. A method according to claim 76, wherein said lack of rigidity is absolute.

78. A method according to claim 76, wherein said lack of rigidity is relative to other potential scaffolds.

79. A method according to claim 76, comprising:

determining a spanning, in chemical configuration space, of said part of a screening library;

determining at least one spatial chemical configuration of said potential molecule; and

selecting said potential gauge molecule if it adds at least one significant spatial chemical configuration to said screening library.

80. A method according to claim 76, wherein providing a set of molecules comprises generating said molecules using a single scaffold to which moieties are selectively attached.

81. A method according to claim 76, wherein providing a set of molecules comprises providing a chemical library.

82. A method according to claim 79, wherein said gauge is selected if it adds at least one spatial chemical configuration not previously provided or overlapping a provided configuration.

83. A method of creating at least a portion of a screening library, comprising:

selecting a scaffold molecule to which moieties can be added;

determining a plurality of potential gauges which can be created by attaching moieties to said scaffold; and

selecting a subset of said gauges that do not substantially overlap in chemical configurations.

84. A method according to claim 83, comprising:

rejecting potential gauges that add over six spatial chemical configurations.

85. A method of reducing a screening library, comprising:

for each molecule in at least part of said library, determining substantially all the spatial chemical configurations of a certain order of binding points provided by the molecule; and

removing a plurality of molecules which add redundant spatial chemical configurations.

86. A method according to claim 85, wherein said certain order is three.

87. A method of reducing a screening library, comprising:

for each molecule in at least part of said library, calculating a binding probability of said molecules based on energetic considerations; and

removing at least some molecules whose binding probability is below a threshold value.

88. A method according to claim 87, wherein said binding probability is calculated using a formula which is inversely dependent on a flexibility of the molecule.

89. A method according to claim 87, wherein said binding probability is at least estimated based on a solubility of the molecule.

90. A method of designing a screening library for a projected target molecule task, comprising:

determining a desired range of distances between binding points to be directly identified by said library;

determining a desired overlap between measures provided by gauge molecules of said library;

determining a set of desired binding types to be discriminated between; and

generating a plurality of gauges, said gauges each defining a plurality of binding types and distances between them, such that said gauges cover a spatial chemical configuration space that includes said distances and said binding types with said desired overlap.

91. A method according to claim 90, wherein generating a plurality of moieties comprises generating by attaching moieties to scaffolds.

92. A method according to claim 90, wherein said gauges cover a spatial chemical configuration space of triplets of binding points.

93. A method according to claim 90, wherein said projected target molecule task comprises proteins.

94. A method according to claim 90, wherein said overlap is at least two.

95. A method according to claim 90, wherein said overlap is at least four.

96. A method according to claim 90, wherein said overlap is at least six.

97. A method according to claim 90, wherein said gauges are substantially rigid.

98. A method according to claim 90, wherein said coverage takes into account an inherent flexibility of binding.

99. A method according to claim 90, wherein generating comprises generating substantially same configurations by different gauges, thereby providing at least part of said overlap.

100. A method according to claim 99, wherein generating comprises providing a repetition factor of at least two.

101. A method according to claim 90, wherein generating comprises generating substantially different configurations by different gauges, which different configurations overlap due to a degree of flexibility thereof, thereby providing at least part of said overlap.

102. A method according to claim 1, comprising generating a set of drug leads for said target based on said information.

103. A method according to claim 102, comprising removing known drug leads for said target from said set.

104. A lead set produced by the method of claim 102.

105. A lead set produced by the method of claim 103.

106. A drug lead comprising:
a plurality of substantially rigid scaffolds molecule sections;
at least one link interconnecting said scaffold molecule sections; and
a plurality of moieties attached to said scaffolds.

107. A screening library comprising:
at least 10,000 molecules generated by attaching moieties to a set of fewer than 50 scaffold molecules.

108. A screening library according to claim 107, wherein fewer than 20 scaffold molecules are used to generate said at least 10,000 molecules.

109. A library according to claim 107, wherein said scaffolds include at least one of the following scaffold molecules: Thiophene; 1H-Pyrrole; Furan; Benzene; Pyridine; Pyrimidine; Pyrazine; 6H-Thieno[2,3-b]pyrrole; 1,6-Dihydro-pyrrolo[2,3-b]pyrrole; 1H-Indole; Thieno[2,3-d]pyrimidine; 6,7-Dihydro-pyrazolo[1,5-a]pyrimidine; Quinoline; Isoquinoline;

Quinoxaline; 3,4-Dihydro-benzo[e][1,4]diazepin-5-one; 3,8-Dihydro-4H-pyrrolo[2,3-e][1,4]diazepin-5-one; 3,4-Dihydro-thieno[2,3-e][1,4]diazepin-5-one; 3,6-Dihydro-4H-pyrrolo[3,2-e][1,4]diazepin-5-one; 5H,11H-Dibenzo[b,f][1,5]diazocine-6,12-dione; 1,4-Dihydro-10H-1,4,10-1,4,10-triaza-benzo[a]cyclopenta[e]cyclooctene-5,11-dione; 4H,10H-1-Thia-4,10-diaza-benzo[a]cyclopenta[e]cyclooctene-5,11-dione; Dipyrrolo[1,2-c;2',1'-e]imidazol-5-one; 1,4,7,9-Tetrahydro-1,4,6,9-tetraaza-dicyclopenta[a,e]cyclooctene-5,10-dione; 4,7,9-Trihydro-1-thia-4,6,9-triaza-dicyclopenta[a,e]cyclooctene-5,10-dione; 2,4,9,Trihydro-1lambda*4*,6-dithia-4,9-diaza-dicyclopenta[a,e]cyclooctene-5,10-dione; 6,9-Dihydro-5H-1-thia-5,8,9,triaza-cyclopenta[a]azulen-4-one; 3,10,Dihydro-4H-[1,4]diazepino[5,6-b]indol-5-one; 3,6-Dihydro-4H-[1,4]diazepino[6,5-b]indol-5-one; 7,8-Dihydro-1H-1,7,10-triaza-cyclohepta[e]inden-6-one; 8,9-Dihydro-3H-3,6,9-triaza-cyclohepta[e]inden-10-one; 7,8-Dihydro-1H-1,5,8-triaza-cyclohepta[f]inden-9-one; 8,9-Dihydro-5,6,9,11-tetraaza-cyclohept[b]naphthalene-10-one; 3,4-Dihydro-[1,4]diazepino[5,6-b]quinolin-5-one; 8,9-Dihydro-4,8,11-triaza-cyclohepta[a]naphthalene-7-one; 11H-10,11-Diaza-benzo[b]fluorine; α-hydroxyacids; α-aminoacids; cohels; Bicyclo[2.2.2]octane; 2-Methylene-2,3-dihydrobenzo[1,4]dioxine; 6,7-Dihydro-2H-pyrazino[1,2-a]pyramidine; 9H-Fluorene; 1,4-Diaza-bictclo[2.2.2]octane; 1-Aza-bicyclo[2.2.2]octane; Pyrido[2,3-d]pyrimidine; 5-Methylene-1,5-dihydro-pyrrol-2-one; Bezno[4,5]imidazo[1,2-a]pyrimidine; 1,4-Dihydro-benzo[4,5]imidazo[1,2-a]pyrimidine; 4,10-Dihydro-1,4a,10-triaza-phenanthren-9-one; 1,5-Dihydro-imidazo[1,2-a]pyrimidin-2-one; 1,2,3,5-Tetrahydro-imidazo[1,2-a]pyrimidine; Thiazolo[3,2-a]thieno[2,3-d]pyrimidin-5-one; 1,9-Dithia-4a,10-diaza-cyclopenta[b]fluoren-4-one; 5,6-Dihydro-1-thia-5,7,8,9a-tetraaza-cyclopenta[e]azulen-4-one; 6,10-Dihydro-5H-1-thia-5,7,10a-triaza-benzo[e]azulen-4-one; 4,5-Dihydro-3-thia-4,5a,10-triaza-cyclopenta[a]fluorine; 8H-1-Thia-cyclopenta[a]indene; 3-Thia-4,5a,10-triaza-cyclopenta[a]fluorine; 6,7,9,11-Tetrahydro-10-thia-6,9-diaza-indeno[1,2-a]azulene-5,8-dione; 2,3,6,7,12a-Hexahydropyrazino[1',2':1,6]pyrido[3,4-b]indole-1,4-dione; 5,10-Dihydro-4H-2,3a,10-triaza-cyclopenta[a]fluorine; 5H-Pyrido[4,3-b]indole; 11H-Indolizino[1,2-b]quinolin-9-one; 1,2-Dihydro-2,4a,9,-triaza-anthracene-3,10-dione; 6H-Isoindolo[2,1-a]indole; 1,5-Dihydro-benzo[b][1,4]diazepin-2-one; 5,10-Dihydro-dibenzo[b,e][1,4]diazepin-11-one; 5,11-Dihydro-benzo[e]pyrido[3,2-b][1,4]diazepin-6-one; 4,9-Dihydro-3-thia-4,9-diaza-benzo[f]azulen-10-one; Benzo[g]quinoxaline; Pyrazino[2,3-b]quinoxaline; Pyrido[2,1-b]quinazolin-11-one; 1-Thia-4a,9-diaza-cyclopenta[b]naphthalene-4-one; 2-Methylene-4H-benzo[1,4]thiazin-3-one.

110. A library according to claim 107, wherein at least 4 of said scaffolds have exactly a single ring.

111. A library according to claim 107, wherein at least 4 of said scaffolds have exactly two rings.

112. A library according to claim 107, wherein at least 4 of said scaffolds have exactly three rings.

113. A library according to claim 107, wherein at least 4 of said scaffolds have exactly four rings.

114. A library according to claim 107, wherein said library includes at least 50,000 thus generated molecules.

115. A library according to claim 107, wherein said library includes at least 100,000 thus generated molecules.

116. A library according to claim 109, wherein said scaffolds include at least three of said following scaffold molecules.

117. A library according to claim 109, wherein said scaffolds include at least ten of said following scaffold molecules.

118. A library according to claim 107, wherein said generated molecules are substantially rigid.

119. A library according to claim 107, wherein said molecules span a configuration space of spatial geometrical patterns of binding point types, including at least 25% of the patterns that exist in protein targets.

120. A library according to claim 119, wherein said molecules span at least 50% of the patterns.

121. A library according to claim 119, wherein said molecules span a space defining at least 4 distinct binding point chemistry types.

122. A library according to claim 119, wherein said molecules span a space defining at least 5 distinct binding point chemistry types.

123. A screening library, comprising:

at least 100 gauge molecules generated by attaching moieties to at least one of the following scaffolds: Thiophene; 1H-Pyrrole; Furan; Benzene; Pyridine; Pyrimidine; Pyrazine; 6H-Thieno[2,3-b]pyrrole; 1,6-Dihydro-pyrrolo[2,3-b]pyrrole; 1H-Indole; Thieno[2,3-d]pyrimidine; 6,7-Dihydro-pyrazolo[1,5-a]pyrimidine; Quinoline; Isoquinoline; Quinoxaline; 3,4-Dihydro-benzo[e][1,4]diazepin-5-one; 3,8-Dihydro-4H-pyrrolo[2,3-e][1,4]diazepin-5-one; 3,4-Dihydro-thieno[2,3-e][1,4]diazepin-5-one; 3,6-Dihydro-4H-pyrrolo[3,2-e][1,4]diazepin-5-one; 5H,11H-Dibenzo[b,f][1,5]diazocine-6,12-dione; 1,4-Dihydro-10H-1,4,10-1,4,10-triaza-benzo[a]cyclopenta[e]cyclooctene-5,11-dione; 4H,10H-1-Thia-4,10-diaza-benzo[a]cyclopenta[e]cyclooctene-5,11-dione; Dipyrrolo[1,2-c;2',1'-e]imidazol-5-one; 1,4,7,9-Tetrahydro-1,4,6,9-tetraaza-dicyclopenta[a,e]cyclooctene-5,10-dione; 4,7,9-Trihydro-1-thia-4,6,9-triaza-dicyclopenta[a,e]cyclooctene-5,10-dione; 2,4,9,Trihydro-1lambda*4*,6-dithia-4,9-diaza-dicyclopenta[a,e]cyclooctene-5,10-dione; 6,9-Dihydro-5H-1-thia-5,8,9,triaza-cyclopenta[a]azulen-4-one; 3,10,Dihydro-4H-[1,4]diazepino[5,6-b]indol-5-one; 3,6-Dihydro-4H-[1,4]diazepino[6,5-b]indol-5-one; 7,8-Dihydro-1H-1,7,10-triaza-cyclohepta[e]inden-6-one; 8,9-Dihydro-3H-3,6,9-triaza-cyclohepta[e]inden-10-one; 7,8-Dihydro-1H-1,5,8-triaza-cyclohepta[f]inden-9-one; 8,9-Dihydro-5,6,9,11-tetraaza-cyclohept[b]naphthalene-10-one; 3,4-Dihydro-[1,4]diazepino[5,6-b]quinolin-5-one; 8,9-Dihydro-4,8,11-triaza-cyclohepta[a]naphthalene-7-one; 11H-10,11-Diaza-benzo[b]fluorine; α-hydroxyacids; α-aminoacids; cohels; Bicyclo[2.2.2]octane; 2-Methylene-2,3-dihydrobenzo[1,4]dioxine; 6,7-Dihydro-2H-pyrazino[1,2-a]pyramidine; 9H-Fluorene; 1,4-Diaza-bictclo[2.2.2]octane; 1-Aza-bicyclo[2.2.2]octane; Pyrido[2,3-d]pyrimidine; 5-Methylene-1,5-dihydro-pyrrol-2-one; Bezno[4,5]imidazo[1,2-a]pyrimidine; 1,4-Dihydro-benzo[4,5]imidazo[1,2-a]pyrimidine; 4,10-Dihydro-1,4a,10-triaza-phenanthren-9-one; 1,5-Dihydro-imidazo[1,2-a]pyrimidin-2-one;

1,2,3,5-Tetrahydro-imidazo[1,2-a]pyrimidine; Thiazolo[3,2-a]thieno[2,3-d]pyrimidin-5-one; 1,9-Dithia-4a,10-diaza-cyclopenta[b]fluoren-4-one; 5,6-Dihydro-1-thia-5,7,8,9a-tetraaza-cyclopenta[e]azulen-4-one; 6,10-Dihydro-5H-1-thia-5,7,10a-triaza-benzo[e]azulen-4-one; 4,5-Dihydro-3-thia-4,5a,10-triaza-cyclopenta[a]fluorine; 8H-1-Thia-cyclopenta[a]indene; 3-Thia-4,5a,10-triaza-cyclopenta[a]fluorine; 6,7,9,11-Tetrahydro-10-thia-6,9-diaza-indeno[1,2-a]azulene-5,8-dione; 2,3,6,7,12a-Hexahydropyrazino[1',2':1,6]pyrido[3,4-b]indole-1,4-dione; 5,10-Dihydro-4H-2,3a,10-triaza-cyclopenta[a]fluorine; 5H-Pyrido[4,3-b]indole; 11H-Indolizino[1,2-b]quinolin-9-one; 1,2-Dihydro-2,4a,9,-triaza-anthracene-3,10-dione; 6H-Isoindolo[2,1-a]indole; 1,5-Dihydro-benzo[b][1,4]diazepin-2-one; 5,10-Dihydro-dibenzo[b,e][1,4]diazepin-11-one; 5,11-Dihydro-benzo[e]pyrido[3,2-b][1,4]diazepin-6-one; 4,9-Dihydro-3-thia-4,9-diaza-benzo[f]azulen-10-one; Benzo[g]quinoxaline; Pyrazino[2,3-b]quinoxaline; Pyrido[2,1-b]quinazolin-11-one; 1-Thia-4a,9-diaza-cyclopenta[b]naphthalene-4-one; 2-Methylene-4H-benzo[1,4]thiazin-3-one.

124. A library according to claim 123, wherein said molecules are generated using at least one of the following scaffolds:
Thiophene; 1H-Pyrrole; Furan; Benzene; Pyridine; Pyrimidine; Pyrazine; 6H-Thieno[2,3-b]pyrrole; 1,6-Dihydro-pyrrolo[2,3-b]pyrrole; 1H-Indole; Thieno[2,3-d]pyrimidine; 6,7-Dihydro-pyrazolo[1,5-a]pyrimidine; Quinoline; Isoquinoline; Quinoxaline; 3,4-Dihydro-benzo[e][1,4]diazepin-5-one; 3,8-Dihydro-4H-pyrrolo[2,3-e][1,4]diazepin-5-one; 3,4-Dihydro-thieno[2,3-e][1,4]diazepin-5-one; 3,6-Dihydro-4H-pyrrolo[3,2-e][1,4]diazepin-5-one; 5H,11H-Dibenzo[b,f][1,5]diazocine-6,12-dione; 1,4-Dihydro-10H-1,4,10-1,4,10-triaza-benzo[a]cyclopenta[e]cyclooctene-5,11-dione; 4H,10H-1-Thia-4,10-diaza-benzo[a]cyclopenta[e]cyclooctene-5,11-dione; Dipyrrolo[1,2-c;2',1'-e]imidazol-5-one.

125. A library according to claim 123, wherein said at least 100 molecules comprise at least 300 molecules.

126. A library according to claim 123, wherein said at least 100 molecules of said library are generated using a single one of said scaffolds.

127. A screening library comprising a set of at least 10,000 substantially rigid molecules.

128. A library according to claim 127, wherein said set comprises at least 50,000 substantially rigid molecules.

129. A library according to claim 127, wherein said set comprises at least 100,000 substantially rigid molecules.

130. A library according to claim 127, wherein said set is selected to have a an expected binding rate of at least 0.1% of the library for protein targets in general.

131. A library according to claim 130, wherein said expected binding rate is at least 0.5%.

132. A library according to claim 130, wherein said set is designed to provide molecules with a uniformity of hit probability for a generalized target of within a ratio of 1:100 for the whole set.

133. A library according to claim 132, wherein said ratio is within 1:10.

134. A library according to claim 127, wherein said set spans a space of spatial chemical configurations, each such configuration defining a certain plurality of binding points having distances between them, the set covering substantially all possible configurations in the space in a given range of distances.

135. A screening library, comprising:

a plurality of at least 5,000 gauge molecules, each such molecule defining at least one spatial configuration of binding type points,

wherein substantially each point in a space of such configurations is covered by at least two different gauge molecules.

136. A library according to claim 135, wherein each point is covered by at least two substantially identical spatial configurations.

137. A library according to claim 135, wherein each point is covered by at least two substantially different spatial configurations.

138. A library according to claim 135, wherein said space is a space of triangles defined by binding type at vertexes and distances between vertexes.

139. A library according to claim 138, wherein said space includes distances of between 4 Å and 8 Å (angstrom $= 10^{-10}$ meters).

140. A library according to claim 138, wherein said space includes distances of between 2 Å and 10 Å.

141. A library according to claim 138, wherein said space includes at least 5 different binding types.

142. A library according to claim 138, wherein said space includes at least 7 different binding types.

143. A library according to claim 138, wherein said space includes omni-directional binding types.

144. A library according to claim 138, wherein said space includes directional binding types.

145. A library according to claim 138, wherein said substantially each point in said space is covered by at least three gauges.

146. A library according to claim 138, wherein substantially all the gauges include a plurality of configurations of said space.

147. A method of obtaining information about a binding behavior of a target molecule, comprising:

providing a set of substantially rigid chemical gauges, a significant number of said gauges being expected to bind with said target;

reacting said target with a plurality of gauges of said set of gauges; and

physically analyzing a structure of said target bound to a gauge.

148. A method according to claim 147, wherein physically analyzing comprises analyzing using NMR.

149. A method according to claim 147, wherein physically analyzing comprises analyzing using X-ray crystallography.

150. A method according to claim 147, wherein physically analyzing comprises analyzing using binding with a set of gauges.

151. A method according to claim 147, comprising virtually super-imposing a plurality of structures obtained by said physically analyzing.

152. A method of constructing a lead, comprising:

providing a set of substantially rigid chemical gauges;

reacting said target with a plurality of gauges of said set of gauges;

assaying a binding of said gauges with said target to obtain a plurality of assay results; and

constructing a lead based on said assay results.

153. A method according to claim 152, wherein constructing a lead comprises linking together a plurality of gauges found to bind in said assaying.

154. A method according to claim 152, wherein constructing a lead comprises modifying an existing molecule to have moieties that correspond to binding locations found by said assaying.